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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/211,312

180
AU 1807-

1213
DATE: 02/09/95
TIME: 12:45:00

INPUT SET: S2235.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: LABIGNE, AGNES
CUSSAC, VALERIE
FERRERO, RICHARD

(ii) TITLE OF INVENTION: GENES OF HELICOBACTER PYLORI NECESSARY
FOR THE REGULATION AND MATURATION OF UREASE AND THEIR USE

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
P.C.

(B) STREET: 1755 S. Jefferson Davis Highway, Suite 400

(C) CITY: Arlington

(D) STATE: Virginia

(E) COUNTRY: U.S.A.

(F) ZIP: 22202

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/211,312

(B) FILING DATE: 01-JUL-1994

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: FR 91 12198

(B) FILING DATE: 03-OCT-1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/FR92/00921

(B) FILING DATE: 02-OCT-1992

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Oblon, Norman F.

(B) REGISTRATION NUMBER: 24,618

(C) REFERENCE/DOCKET NUMBER: 660-075-0XPCT

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47 (ix) TELECOMMUNICATION INFORMATION:
48 (A) TELEPHONE: (703) 413-3000
49 (B) TELEFAX: (703) 413-2220
50 (C) TELEX: 248855 OPAT UR
51
52
53 (2) INFORMATION FOR SEQ ID NO:1:
54
55 (i) SEQUENCE CHARACTERISTICS:
56 (A) LENGTH: 3559 base pairs
57 (B) TYPE: nucleic acid
58 (C) STRANDEDNESS: unknown
59 (D) TOPOLOGY: unknown
60
61 (ii) MOLECULE TYPE: DNA (genomic)
62
63
64 (ix) FEATURE:
65 (A) NAME/KEY: CDS
66 (B) LOCATION: 2..16
67
68 (ix) FEATURE:
69 (A) NAME/KEY: CDS
70 (B) LOCATION: 211..795
71
72 (ix) FEATURE:
73 (A) NAME/KEY: CDS
74 (B) LOCATION: 800..1309
75
76 (ix) FEATURE:
77 (A) NAME/KEY: CDS
78 (B) LOCATION: 1324..2091
79
80 (ix) FEATURE:
81 (A) NAME/KEY: CDS
82 (B) LOCATION: 2122..2718
83
84 (ix) FEATURE:
85 (A) NAME/KEY: CDS
86 (B) LOCATION: 2721..3515
87
88
89 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
90
91 A CTC TTT AGC ATT TTC TAGGATTTTT TAGGAGCAAC GCTCTTAGAT CCTTAGTTTT 56
92 Leu Phe Ser Ile Phe
93 1 5
94
95 TAGCTCTCTG ATTTTTTGTT TATCAAAAAA TTGGGGGCTT TTTTGTTTT TATTTTTTGT 116
96
97 CAATTTACTA TTTTCTTTA TGATTAGCTC AAGCAACAAA AGTTATTCGT AAGGTGCGTT 176
98
99 TGTTGTAAAA ATTTTTGTTT GGAAGGAAAA GGCA ATG CTA GGA CTT GTA TTG 228

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100		Met	Leu	Gly	Leu	Val	Leu													
101		1					5													
102																				
103	TTA	TAT	GTT	GGG	ATT	GTT	TTA	ATC	AGC	AAT	GGG	ATT	TGC	GGG	TTA	ACC				276
104	Leu	Tyr	Val	Gly	Ile	Val	Leu	Ile	Ser	Asn	Gly	Ile	Cys	Gly	Leu	Thr				
105				10					15					20						
106																				
107	AAA	GTC	GAT	CCT	AAA	AGC	ACT	GCG	GTG	ATG	AAC	TTT	TTT	GTG	GGT	GGG				324
108	Lys	Val	Asp	Pro	Lys	Ser	Thr	Ala	Val	Met	Asn	Phe	Phe	Val	Gly	Gly				
109			25					30					35							
110																				
111	CTC	TCC	ATT	ATT	TGT	AAT	GTG	GTT	GTC	ATC	ACT	TAT	TCC	GCT	CTC	AAC				372
112	Leu	Ser	Ile	Ile	Cys	Asn	Val	Val	Val	Ile	Thr	Tyr	Ser	Ala	Leu	Asn				
113		40					45					50								
114																				
115	CCT	ACA	GCC	CCT	GTA	GAA	GGT	GCT	GAA	GAT	ATT	GCT	CAA	GTA	TCA	CAC				420
116	Pro	Thr	Ala	Pro	Val	Glu	Gly	Ala	Glu	Asp	Ile	Ala	Gln	Val	Ser	His				
117		55				60					65				70					
118																				
119	CAT	TTG	ACT	AAT	TTC	TAT	GGG	CCA	GCG	ACT	GGG	TTA	TTG	TTT	GGT	TTC				468
120	His	Leu	Thr	Asn	Phe	Tyr	Gly	Pro	Ala	Thr	Gly	Leu	Leu	Phe	Gly	Phe				
121				75						80					85					
122																				
123	ACC	TAC	TTG	TAT	GCG	GCT	ATC	AAC	CAC	ACT	TTT	GGT	TTG	GAT	TGG	AGG				516
124	Thr	Tyr	Leu	Tyr	Ala	Ala	Ile	Asn	His	Thr	Phe	Gly	Leu	Asp	Trp	Arg				
125			90					95					100							
126																				
127	CCC	TAC	TCT	TGG	TAT	AGC	TTA	TTC	GTA	GCG	ATC	AAC	ACG	ATT	CCT	GCT				564
128	Pro	Tyr	Ser	Trp	Tyr	Ser	Leu	Phe	Val	Ala	Ile	Asn	Thr	Ile	Pro	Ala				
129			105				110						115							
130																				
131	GCG	ATT	TTA	TCC	CAC	TAT	AGC	GAT	ATG	CTT	GAT	GAC	CAC	AAA	GTG	TTA				612
132	Ala	Ile	Leu	Ser	His	Tyr	Ser	Asp	Met	Leu	Asp	Asp	His	Lys	Val	Leu				
133		120					125					130								
134																				
135	GGC	ATC	ACT	GAA	GGC	GAT	TGG	TGG	GCG	ATC	ATT	TGG	TTG	GCT	TGG	GGT				660
136	Gly	Ile	Thr	Glu	Gly	Asp	Trp	Trp	Ala	Ile	Ile	Trp	Leu	Ala	Trp	Gly				
137	135					140					145				150					
138																				
139	GTT	TTG	TGG	CTT	ACC	GCT	TTC	ATT	GAA	AAC	ATC	TTG	AAA	ATC	CCT	TTA				708
140	Val	Leu	Trp	Leu	Thr	Ala	Phe	Ile	Glu	Asn	Ile	Leu	Lys	Ile	Pro	Leu				
141				155						160					165					
142																				
143	GGG	AAA	TTC	ACT	CCA	TGG	CTT	GCT	ATC	ATT	GAG	GGC	ATT	TTA	ACC	GCT				756
144	Gly	Lys	Phe	Thr	Pro	Trp	Leu	Ala	Ile	Ile	Glu	Gly	Ile	Leu	Thr	Ala				
145			170					175					180							
146																				
147	TGG	ATC	CCT	GCT	TGG	TTA	CTC	TTT	ATC	CAA	CAC	TGG	GTG	TGAG	ATG	ATC				805
148	Trp	Ile	Pro	Ala	Trp	Leu	Leu	Phe	Ile	Gln	His	Trp	Val		Met	Ile				
149			185				190						195		1					
150																				
151	ATA	GAG	CGT	TTA	ATA	GGC	AAT	CTA	AGG	GAT	TTA	AAC	CCC	TTG	GAT	TTC				853
152	Ile	Glu	Arg	Leu	Ile	Gly	Asn	Leu	Arg	Asp	Leu	Asn	Pro	Leu	Asp	Phe				

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	5	10	15	
153				
154				
155	AGC GTG GAT TAT GTG GAT TTG GAA TGG TTT GAA ACG AGG AAA AAA ATC			901
156	Ser Val Asp Tyr Val Asp Leu Glu Trp Phe Glu Thr Arg Lys Lys Ile			
157	20	25	30	
158				
159	GCT CGC TTT AAA ACC AGG CAA GGC AAA GAC ATA GCC GTA CGC CTT AAA			949
160	Ala Arg Phe Lys Thr Arg Gln Gly Lys Asp Ile Ala Val Arg Leu Lys			
161	35	40	45	50
162				
163	GAC GCT CCC AAG TTG GGT TTC TCT CAA GGA GAT ATT TTA TTT AAA GAA			997
164	Asp Ala Pro Lys Leu Gly Phe Ser Gln Gly Asp Ile Leu Phe Lys Glu			
165	55	60	65	
166				
167	GAG AAG GAA ATT ATC GCC GTT AAT ATC TTG GAT TCT GAA GTC ATT CAC			1045
168	Glu Lys Glu Ile Ile Ala Val Asn Ile Leu Asp Ser Glu Val Ile His			
169	70	75	80	
170				
171	ATC CAA GCT AAG AGC GTG GCA GAA GTA GCG AAA ATA TGC TAT GAA ATA			1093
172	Ile Gln Ala Lys Ser Val Ala Glu Val Ala Lys Ile Cys Tyr Glu Ile			
173	85	90	95	
174				
175	GGA AAC CGC CAT GCG GCT TTA TAC TAT GGC GAG TCT CAA TTT GAA TTT			1141
176	Gly Asn Arg His Ala Ala Leu Tyr Tyr Gly Glu Ser Gln Phe Glu Phe			
177	100	105	110	
178				
179	AAA ACA CCA TTT GAA AAG CCC ACG CTA GCG TTA CTA GAA AAG CTA GGG			1189
180	Lys Thr Pro Phe Glu Lys Pro Thr Leu Ala Leu Leu Glu Lys Leu Gly			
181	115	120	125	130
182				
183	GTT CAA AAT CGT GTT TTA AGT TCA AAA TTG GAT TCC AAA GAA CGC TTA			1237
184	Val Gln Asn Arg Val Leu Ser Ser Lys Leu Asp Ser Lys Glu Arg Leu			
185	135	140	145	
186				
187	ACC GTG AGC ATG CCC CAT AGT GAG CCT AAT TTT AAG GTC TCA CTG GCG			1285
188	Thr Val Ser Met Pro His Ser Glu Pro Asn Phe Lys Val Ser Leu Ala			
189	150	155	160	
190				
191	AGC GAT TTT AAA GTG GTC ATG AAA TAGAAAAACA ACAA ATG GAT AAA GGA			1335
192	Ser Asp Phe Lys Val Val Met Lys		Met Asp Lys Gly	
193	165	170	1	
194				
195	AAA AGC GTG AAA AGC ATT GAA AAA AGC GTG GGT ATG CTC CCA AAA ACT			1383
196	Lys Ser Val Lys Ser Ile Glu Lys Ser Val Gly Met Leu Pro Lys Thr			
197	5	10	15	20
198				
199	CCA AAG ACA GAC AGC AAT GCT CAT GTG GAT AAT GAA TTT CTG ATT CTG			1431
200	Pro Lys Thr Asp Ser Asn Ala His Val Asp Asn Glu Phe Leu Ile Leu			
201	25	30	35	
202				
203	CAA GTC AAT GAT GCG GTG TTC CCC ATT GGA TCT TAC ACG CAT TCT TTT			1479
204	Gln Val Asn Asp Ala Val Phe Pro Ile Gly Ser Tyr Thr His Ser Phe			
205	40	45	50	

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206																		
207	GGG	CTT	TTG	GCT	AGA	AAC	TTA	CAT	CCA	GCA	AAA	AAG	GTT	ACT	AAT	AAA		
208	Gly	Leu	Leu	Ala	Arg	Asn	Leu	His	Pro	Ala	Lys	Lys	Val	Thr	Asn	Lys		1527
209			55					60					65					
210																		
211	GAA	AGC	GCT	TTA	AAA	TAT	TTA	AAA	GCC	AAT	CTC	TCT	AGC	CAG	TTC	CTT		
212	Glu	Ser	Ala	Leu	Lys	Tyr	Leu	Lys	Ala	Asn	Leu	Ser	Ser	Gln	Phe	Leu		1575
213		70					75					80						
214																		
215	TAC	ACG	GAA	ATG	CTG	AGC	TTG	AAA	CTC	ACC	TAT	GAA	AGC	GCT	CTC	CAA		
216	Tyr	Thr	Glu	Met	Leu	Ser	Leu	Lys	Leu	Thr	Tyr	Glu	Ser	Ala	Leu	Gln		1623
217		85				90					95					100		
218																		
219	CAA	GAT	TTA	AAA	AGG	ATC	TTA	GGG	GTT	GAA	GAA	ATC	ATT	ACG	CTA	TCC		
220	Gln	Asp	Leu	Lys	Arg	Ile	Leu	Gly	Val	Glu	Glu	Ile	Ile	Thr	Leu	Ser		1671
221					105					110					115			
222																		
223	ACA	AGC	CCC	ATG	GAA	TTG	CGA	TTA	GCC	AAT	CAA	AAG	CTA	GGC	AAT	CGT		
224	Thr	Ser	Pro	Met	Glu	Leu	Arg	Leu	Ala	Asn	Gln	Lys	Leu	Gly	Asn	Arg		1719
225				120					125					130				
226																		
227	TTC	ATT	AAA	ACC	TTA	CAA	GCC	ATG	AAC	GAA	TTA	GAC	ATT	GGC	GCA	TTT		
228	Phe	Ile	Lys	Thr	Leu	Gln	Ala	Met	Asn	Glu	Leu	Asp	Ile	Gly	Ala	Phe		1767
229			135				140						145					
230																		
231	TTT	AAC	GCT	TAC	GCT	CAA	CAA	ACC	GAA	GAC	CCC	ACC	CAT	GCC	ACT	AGC		
232	Phe	Asn	Ala	Tyr	Ala	Gln	Gln	Thr	Glu	Asp	Pro	Thr	His	Ala	Thr	Ser		1815
233		150					155					160						
234																		
235	TAT	GGC	GTT	TTT	GCG	GCG	AGT	TTG	GGG	ATT	GAA	TTG	AAA	AAG	GCT	TTA		
236	Tyr	Gly	Val	Phe	Ala	Ala	Ser	Leu	Gly	Ile	Glu	Leu	Lys	Lys	Ala	Leu		1863
237		165				170					175					180		
238																		
239	AGG	CAT	TAT	CTT	TAT	GCA	CAA	ACT	TCT	AAC	ATG	GTA	ATT	AAC	TGC	GTT		
240	Arg	His	Tyr	Leu	Tyr	Ala	Gln	Thr	Ser	Asn	Met	Val	Ile	Asn	Cys	Val		1911
241					185					190					195			
242																		
243	AAA	AGC	GTC	CCA	CTA	TCT	CAA	AAC	GAT	GGG	CAA	AAA	ATC	TTA	TTG	AGC		
244</																		

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SEQUENCE VERIFICATION REPORT
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